

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT:  
(A) NAME: Federal Republic of Germany, ultimately represented by the Director of the Robert-Koch-Institut  
(B) STREET: Nordufer 20  
(C) CITY: Berlin  
10 (D) STATE OR PROVINCE: Berlin  
(E) COUNTRY: Germany  
(F) POSTAL CODE: 13353

15 (ii) TITLE OF INVENTION: Costimulating polypeptide of T cells, monoclonal antibodies, and the preparation and use thereof

(iii) NUMBER OF SEQUENCES: 4

20 (iv) COMPUTER-READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:  
APPLICATION NUMBER:

(2) INFORMATION FOR SEQ ID NO: 1:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2641 base pairs  
(B) TYPE: Nucleotides  
35 (C) STRANDEDNESS: Double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

40 CGAGAGCCTG AATTCAGTGT CAGCTTTGAA CACTGAACGC GAGGACTGTT AACTGTTTCT 60  
GGCAAACATG AAGTCAGGCC TCTGGTATTT CTTTCTCTTC TGCTTGCACA TTAAGTTTT 120  
AACAGGAGAA ATCAATGGTT CTGCCAATTA TGAGATGTTT ATATTTACA ACGGAGGTGT 180  
ACAAATTTTA TGCAAATATC CTGACATTGT CCAGCAATTT AAAATGCAGT TGCTGAAAGG 240  
GGGGCAAATA CTCTGCGATC TCACTAAGAC AAAAGGAAGT GGAAACACAG TGTCCATTAA 300  
GAGTCTGAAA TTCTGCCATT CTCAGTTATC CAACAACAGT GTCTCTTTTT TTCTATACAA 360  
CTTGGACCAT TCTCATGCCA ACTATTACTT CTGCAACCTA TCAATTTTGT ATCCTCCTCC 420  
TTTTAAAGTA ACTCTTACAG GAGGATATTT GCATATTTAT GAATCACAAC TTTGTTGCCA 480  
GCTGAAGTTC TGGTTACCCA TAGGATGTGC AGCCTTTGTT GTAGTCTGCA TTTTGGGATG 540  
CATACTTATT TGTTGGCTTA CAAAAAGAA GTATTCATCC AGTGTGCACG ACCCTAACGG 600

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TGAATACATG TTCATGAGAG CAGTGAACAC AGCCAAAAA TCTAGACTCA CAGATGTGAC	660
CCTATAATAT GGAACCTCTGG CACCCAGGCA TGAAGCACGT TGGCCAGTTT TCCTCAACTT	720
GAAGTGCAAG ATTCTCTTAT TTCCGGGACC ACGGAGAGTC TGACTTAACT ACATACATCT	780
TCTGCTGGTG TTTTGTTCAA TCTGGAAGAA TGACTGTATC AGTCAATGGG GATTTTAAAC	840
GACTGCTTGG GTACTGCCGA GTCCTCTCAA AACAAACACC CTCTTGCAAC CAGCTTTGGA	900
GAAAGCCCAG CTCCTGTGTG CTCACTGGGA GTGGAATCCC TGTCTCCACA TCTGCTCCTA	960
GCACTGCATC AGCCAGTAAA ACAAACACAT TTACAAGAAA AATGTTTTAA AGATGCCAGG	1020
GGTACTGAAT CTGCAAAGCA AATGAGCAGC CAAGGACCAG CATCTGTCCG CATTTCACTA	1080
TCATACTACC TCTTCTTTCT GTAGGGATGA GAATTCCTCT TTTAATCAGT CAAGGGAGAT	1140
GCTTCAAAGC TGGAGCTATT TTATTCTGA GATGTTGATG TGAAGTGTAC ATTAGTACAT	1200
ACTCAGTACT CTCCTTCAAT TGCTGAACCC CAGTTGACCA TTTTACCAAG ACTTTAGATG	1260
CTTTCTTGTG CCCTCAATTT TCTTTTAAA AATACTTCTA CATGACTGCT TGACAGCCCA	1320
ACAGCCACTC TCAATAGAGA GCTATGTCTT ACATTCTTTC CTCTGCTGCT CAATAGTTTT	1380
ATATATCTAT GCATACATAT ATACAACAT ATGTATATAA AATTCATAAT GAATATATTT	1440
GCCTATATTC TCCCTACAAG AATATTTTGG CTCCAGAAAG ACATGTTCTT TTCTCAAATT	1500
CAGTTAAAT GGTTTACTTT GTTCAAGTTA GTGGTAGGAA ACATTGCCCG GAATTGAAAG	1560
CAAATTTATT TTATTATCCT ATTTTCTACC ATATCTATG TTTTCATGGT GCTATTAATT	1620
ACAAGTTTAG TTCTTTTGT AGATCATATT AAAATTGCAA ACAAATCAT CTTTAATGGG	1680
CCAGCATTCT CATGGGGTAG AGCAGAATAT TCATTTAGCC TGAAAGCTGC AGTTACTATA	1740
GGTTGCTGTC AGACTATACC CATGGTGCCT CTGGGCTTGA CAGGTCAAAA TGGTCCCCAT	1800
CAGCCTGGAG CAGCCCTCCA GACCTGGGTG GAATTCAGG GTTGAGAGAC TCCCCTGAGC	1860
CAGAGGCCAC TAGGTATTCT TGCTCCCAGA GGCTGAAGTC ACCCTGGGAA TCACAGTGGT	1920
CTACCTGCAT TCATAATTCC AGGATCTGTG AAGAGCACAT ATGTGTCAGG GCACAATTCC	1980
CTCTCATAAA AACCACACAG CCTGGAAATT GGCCCTGGCC CTTCAAGATA GCCTTCTTTA	2040
GAATATGATT TGGCTAGAAA GATTCTTAAA TATGTGGAAT ATGATTATTC TTAGCTGGAA	2100
TATTTTCTCT ACTTCTGTC TGCATGCCCA AGGCTTCTGA AGCAGCCAAT GTCGATGCAA	2160
CAACATTTGT AACTTTAGGT AACTGGGAT TATGTTGTAG TTTAACATTT TGTAAGTGTG	2220
TGCTTATAGT TTACAAGTGA GACCCGATAT GTCATTATGC ATACTTATAT TATCTTAAGC	2280
ATGTGTAATG CTGGATGTGT ACAGTACAGT ACTGAACTTG TAATTTGAAT CTAGTATGTT	2340
GTTCTGTTTT CAGCTGACTT GGACAACCTG ACTGGCTTTG CACAGGTGTT CCCTGAGTTG	2400
TTTGCAGGTT TCTGTGTGTG GGGTGGGGTA TGGGGAGGAG AACCTTCATG GTGGCCCAAC	2460
TGGCCTGGTT GTCCAAGCTG TGCCCTGACA CATCTCATC CCCAGCATGG GACACCTCAA	2520

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GATGAATAAT AATTCACAAA ATTCTGTGA AATCAAATCC AGTTTAAAGA GGAGCCACTT 2580  
ATCAAAGAGA TTTTAACAGT AGTAAGAAGG CAAAGAATAA ACATTGATA TTCAGCAACT 2640  
G 2641

(2) INFORMATION FOR SEQ ID NO: 2:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 199 amino acids  
(B) TYPE: Amino acid  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys  
1 5 10 15  
Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile  
20 25 30  
Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val  
35 40 45  
Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp  
50 55 60  
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu  
65 70 75 80  
Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
85 90 95  
Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser  
100 105 110  
Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu  
115 120 125  
His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro  
130 135 140  
Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu  
145 150 155 160  
Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro  
165 170 175  
Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser  
180 185 190  
Arg Leu Thr Asp Val Thr Leu  
195

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(2) INFORMATION FOR SEQ ID NO: 3:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: Nucleotides  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA  
10 (iii) HYPOTHETICAL: Yes  
(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

MGNCTSACNG AYGTNAC 17

15 (2) INFORMATION FOR SEQ ID NO: 4:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: Nucleotides  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA  
(iii) HYPOTHETICAL: Yes  
(iv) ANTISENSE: NO

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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